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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Lee, Wen-Hwa  
Shepard, H. Michael  
Gregory, Richard J.  
Wills, Ken N.  
Maneval, Daniel C.  
Lee, Eva  
Goodrich, David  
Wang, Nan-Ping
- (ii) TITLE OF INVENTION: Cell Cycle Controlling Compositions and Methods of Use
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Townsend and Townsend and Crew LLP
  - (B) STREET: Two Embarcadero Center, Eighth Floor
  - (C) CITY: San Francisco
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/472,760
  - (B) FILING DATE: 07-JUN-1995
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/951,947
  - (B) FILING DATE: 28-SEP-1992
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/276,041
  - (B) FILING DATE: 14-JUL-1994
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/764,714
  - (B) FILING DATE: 24-SEP-1991
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/265,829
  - (B) FILING DATE: 31-OCT-1988
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/225,099
  - (B) FILING DATE: 08-APR-1994
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/079,207
  - (B) FILING DATE: 17-JUN-1993

(vii) PRIOR APPLICATION DATA:  
    (A) APPLICATION NUMBER: US 07/914,039  
    (B) FILING DATE: 14-JUL-1992

(vii) PRIOR APPLICATION DATA:  
    (A) APPLICATION NUMBER: US 07/550,877  
    (B) FILING DATE: 11-JUL-1990

(vii) PRIOR APPLICATION DATA:  
    (A) APPLICATION NUMBER: US 08/058,784  
    (B) FILING DATE: 07-MAY-1993

(vii) PRIOR APPLICATION DATA:  
    (A) APPLICATION NUMBER: US 07/906,008  
    (B) FILING DATE: 26-JUN-1992

(vii) PRIOR APPLICATION DATA:  
    (A) APPLICATION NUMBER: US 07/553,905  
    (B) FILING DATE: 16-JUL-1990

(vii) PRIOR APPLICATION DATA:  
    (A) APPLICATION NUMBER: US 08/306,513  
    (B) FILING DATE: 13-SEP-1994

(vii) PRIOR APPLICATION DATA:  
    (A) APPLICATION NUMBER: US 08/121,108  
    (B) FILING DATE: 13-SEP-1993

(vii) PRIOR APPLICATION DATA:  
    (A) APPLICATION NUMBER: US 07/956,472  
    (B) FILING DATE: 02-OCT-1992

(vii) PRIOR APPLICATION DATA:  
    (A) APPLICATION NUMBER: US 08/126,810  
    (B) FILING DATE: 24-SEP-1993

(vii) PRIOR APPLICATION DATA:  
    (A) APPLICATION NUMBER: US 07/778,510  
    (B) FILING DATE: 17-OCT-1991

(viii) ATTORNEY/AGENT INFORMATION:  
    (A) NAME: Bastian, Kevin L.  
    (B) REGISTRATION NUMBER: 34,774  
    (C) REFERENCE/DOCKET NUMBER: 17726A-000410US

(ix) TELECOMMUNICATION INFORMATION:  
    (A) TELEPHONE: (415) 576-0200  
    (B) TELEFAX: (415) 576-0300

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 2994 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 139..2922  
 (D) OTHER INFORMATION: /product= "RB protein"  
 /note= "retinoblastoma (RB) gene"

## (ix) FEATURE:

(A) NAME/KEY: -  
 (B) LOCATION: 1273..2922  
 (D) OTHER INFORMATION: /note= "truncated RB protein fragment  
 p56-RB"

## (ix) FEATURE:

(A) NAME/KEY: -  
 (B) LOCATION: 2887..2922  
 (D) OTHER INFORMATION: /note= "RB protein C-terminal peptide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTGTAA CGGGAGTCGG GAGAGGACGG	60
GGCGTGCCCC GCGTGCGCGC GCGTCGTCCT CCCCGGCGCT CCTCCACAGC TCGCTGGCTC	120
CCGCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC	171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala	
1 5 10	
ACC GCC GCC GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC	219
Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro	
15 20 25	
CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT	267
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro	
30 35 40	
CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA	315
Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala	
45 50 55	
TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG	363
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp	
60 65 70 75	
TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT	411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr	
80 85 90	
ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA	459
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	
95 100 105	
GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC	507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
110 115 120	
ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT	555
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
125 130 135	

ACC Thr 140	AGT Ser	ACC Thr	AAA Lys	GTT Val	GAT Asp 145	AAT Asn	GCT Ala	ATG Met	TCA Ser	AGA Arg 150	CTG Leu	TTG Leu	AAG Lys	AAG Lys	TAT Tyr 155	603
GAT Asp	GTA Val	TTG Leu	TTT Phe	GCA Ala 160	CTC Leu	TTC Phe	AGC Ser	AAA Lys	TTG Leu 165	GAA Glu	AGG Arg	ACA Thr	TGT Cys	GAA Glu 170	CTT Leu	651
ATA Ile	TAT Tyr	TTG Leu	ACA Thr 175	CAA Gln	CCC Pro	AGC Ser	AGT Ser	TCG Ser 180	ATA Ile	TCT Ser	ACT Thr	GAA Glu	ATA Ile	AAT Asn	TCT Ser	699
GCA Ala	TTG Leu	GTG Val 190	CTA Leu	AAA Lys	GTT Val	TCT Ser	TGG Trp 195	ATC Ile	ACA Thr	TTT Phe	TTA Leu 200	TTA Leu	GCT Ala	AAA Lys	GGG Gly	747
GAA Glu 205	GTA Val	TTA Leu	CAA Gln	ATG Met	GAA Glu	GAT Asp 210	GAT Asp	CTG Leu	GTG Val	ATT Ile	TCA Ser 215	TTT Phe	CAG Gln	TTA Leu	ATG Met	795
CTA Leu 220	TGT Cys	GTC Val	CTT Leu	GAC Asp	TAT Tyr 225	TTT Phe	ATT Ile	AAA Lys	CTC Leu	TCA Ser 230	CCT Pro	CCC Pro	ATG Met	TTG Leu	CTC Leu 235	843
AAA Lys	GAA Glu	CCA Pro	TAT Tyr 240	AAA Lys	ACA Thr	GCT Ala	GTT Val	ATA Ile	CCC Pro 245	ATT Ile	AAT Asn	GGT Gly	TCA Ser	CCT Pro	CGA Arg 250	891
ACA Thr	CCC Pro	AGG Arg	CGA Arg 255	GGT Gly	CAG Gln	AAC Asn	AGG Arg	AGT Ser 260	GCA Ala	CGG Arg	ATA Ile	GCA Ala	AAA Lys 265	CAA Gln	CTA Leu	939
GAA Glu	AAT Asn 270	GAT Asp	ACA Thr	AGA Arg	ATT Ile	ATT Ile	GAA Glu 275	GTT Val	CTC Leu	TGT Cys	AAA Lys 280	GAA Glu	CAT His	GAA Glu	TGT Cys	987
AAT Asn 285	ATA Ile	GAT Asp	GAG Glu	GTG Val	AAA Lys	AAT Asn 290	GTT Val	TAT Tyr	TTC Phe	AAA Lys 295	AAT Asn	TTT Phe	ATA Ile	CCT Pro	TTT Phe	1035
ATG Met 300	AAT Asn	TCT Ser	CTT Leu	GGA Gly	CTT Leu 305	GTA Val	ACA Thr	TCT Ser	AAT Asn	GGA Gly 310	CTT Leu	CCA Pro	GAG Glu	GTT Val	GAA Glu 315	1083
AAT Asn	CTT Leu	TCT Ser	AAA Lys	CGA Arg 320	TAC Tyr	GAA Glu	GAA Glu	ATT Ile	TAT Tyr 325	CTT Leu	AAA Lys	AAT Asn	AAA Lys	GAT Asp 330	CTA Leu	1131
GAT Asp	GCA Ala	AGA Arg	TTA Leu 335	TTT Phe	TTG Leu	GAT Asp	CAT His	GAT Asp 340	AAA Lys	ACT Thr	CTT Leu	CAG Gln	ACT Thr 345	GAT Asp	TCT Ser	1179
ATA Ile	GAC Asp 350	AGT Ser	TTT Phe	GAA Glu	ACA Thr	CAG Gln	AGA Arg 355	ACA Thr	CCA Pro	CGA Arg	AAA Lys 360	AGT Ser	AAC Asn	CTT Leu	GAT Asp	1227
GAA Glu 365	GAG Glu	GTG Val	AAT Asn	GTA Val	ATT Ile	CCT Pro 370	CCA Pro	CAC His	ACT Thr	CCA Pro 375	GTT Val	AGG Arg	ACT Thr	GTT Val	ATG Met	1275
AAC	ACT	ATC	CAA	CAA	TTA	ATG	ATG	ATT	TTA	AAT	TCA	GCA	AGT	GAT	CAA	1323

Asn 380	Thr	Ile	Gln	Gln	Leu 385	Met	Met	Ile	Leu	Asn 390	Ser	Ala	Ser	Asp	Gln 395	
CCT Pro	TCA Ser	GAA Glu	AAT Asn	CTG Leu	ATT Ile	TCC Ser	TAT Tyr	TTT Phe	AAC Asn	AAC Asn	TGC Cys	ACA Thr	GTG Val	AAT Asn	CCA Pro	1371
AAA Lys	GAA Glu	AGT Ser	ATA Ile	CTG Leu	AAA Lys	AGA Arg	GTG Val	AAG Lys	GAT Asp	ATA Ile	GGA Gly	TAC Tyr	ATC Ile	TTT Phe	AAA Lys	1419
GAG Glu	AAA Lys	TTT Phe	GCT Ala	AAA Lys	GCT Ala	GTG Val	GGA Gly	CAG Gln	GGT Gly	TGT Cys	GTC Val	GAA Glu	ATT Ile	GGA Gly	TCA Ser	1467
CAG Gln	CGA Arg	TAC Tyr	AAA Lys	CTT Leu	GGA Gly	GTT Val	CGC Arg	TTG Leu	TAT Tyr	TAC Tyr	CGA Arg	GTA Val	ATG Met	GAA Glu	TCC Ser	1515
ATG Met	CTT Leu	AAA Lys	TCA Ser	GAA Glu	GAA Glu	GAA Glu	CGA Arg	TTA Leu	TCC Ser	ATT Ile	CAA Gln	AAT Asn	TTT Phe	AGC Ser	AAA Lys	1563
CTT Leu	CTG Leu	AAT Asn	GAC Asp	AAC Asn	ATT Ile	TTT Phe	CAT His	ATG Met	TCT Ser	TTA Leu	TTG Leu	GCG Ala	TGC Cys	GCT Ala	CTT Leu	1611
GAG Glu	GTT Val	GTA Val	ATG Met	GCC Ala	ACA Thr	TAT Tyr	AGC Ser	AGA Arg	AGT Ser	ACA Thr	TCT Ser	CAG Gln	AAT Asn	CTT Leu	GAT Asp	1659
TCT Ser	GGA Gly	ACA Thr	GAT Asp	TTG Leu	TCT Ser	TTC Phe	CCA Pro	TGG Trp	ATT Ile	CTG Leu	AAT Asn	GTG Val	CTT Leu	AAT Asn	TTA Leu	1707
AAA Lys	GCC Ala	TTT Phe	GAT Asp	TTT Phe	TAC Tyr	AAA Lys	GTG Val	ATC Ile	GAA Glu	AGT Ser	TTT Phe	ATC Ile	AAA Lys	GCA Ala	GAA Glu	1755
GGC Gly	AAC Asn	TTG Leu	ACA Thr	AGA Arg	GAA Glu	ATG Met	ATA Ile	AAA Lys	CAT His	TTA Leu	GAA Glu	CGA Arg	TGT Cys	GAA Glu	CAT His	1803
CGA Arg	ATC Ile	ATG Met	GAA Glu	TCC Ser	CTT Leu	GCA Ala	TGG Trp	CTC Leu	TCA Ser	GAT Asp	TCA Ser	CCT Pro	TTA Leu	TTT Phe	GAT Asp	1851
CTT Leu	ATT Ile	AAA Lys	CAA Gln	TCA Ser	AAG Lys	GAC Asp	CGA Arg	GAA Glu	GGA Gly	CCA Pro	ACT Thr	GAT Asp	CAC His	CTT Leu	GAA Glu	1899
TCT Ser	GCT Ala	TGT Cys	CCT Pro	CTT Leu	AAT Asn	CTT Leu	CCT Pro	CTC Leu	CAG Gln	AAT Asn	AAT Asn	CAC His	ACT Thr	GCA Ala	GCA Ala	1947
GAT Asp	ATG Met	TAT Tyr	CTT Leu	TCT Ser	CCT Pro	GTA Val	AGA Arg	TCT Ser	CCA Pro	AAG Lys	AAA Lys	AAA Lys	GGT Gly	TCA Ser	ACT Thr	1995
ACG Thr	CGT Arg	GTA Val	AAT Asn	TCT Ser	ACT Thr	GCA Ala	AAT Asn	GCA Ala	GAG Glu	ACA Thr	CAA Gln	GCA Ala	ACC Thr	TCA Ser	GCC Ala	2043

620	625					630					635					
TTC	CAG	ACC	CAG	AAG	CCA	TTG	AAA	TCT	ACC	TCT	CTT	TCA	CTG	TTT	TAT	2091
Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	
				640					645					650		
AAA	AAA	GTG	TAT	CGG	CTA	GCC	TAT	CTC	CGG	CTA	AAT	ACA	CTT	TGT	GAA	2139
Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	
			655					660					665			
CGC	CTT	CTG	TCT	GAG	CAC	CCA	GAA	TTA	GAA	CAT	ATC	ATC	TGG	ACC	CTT	2187
Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	
		670					675					680				
TTC	CAG	CAC	ACC	CTG	CAG	AAT	GAG	TAT	GAA	CTC	ATG	AGA	GAC	AGG	CAT	2235
Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	
	685					690					695					
TTG	GAC	CAA	ATT	ATG	ATG	TGT	TCC	ATG	TAT	GGC	ATA	TGC	AAA	GTG	AAG	2283
Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	
700					705					710					715	
AAT	ATA	GAC	CTT	AAA	TTC	AAA	ATC	ATT	GTA	ACA	GCA	TAC	AAG	GAT	CTT	2331
Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	
				720					725					730		
CCT	CAT	GCT	GTT	CAG	GAG	ACA	TTC	AAA	CGT	GTT	TTG	ATC	AAA	GAA	GAG	2379
Pro	His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	
			735					740					745			
GAG	TAT	GAT	TCT	ATT	ATA	GTA	TTC	TAT	AAC	TCG	GTC	TTC	ATG	CAG	AGA	2427
Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	
		750					755					760				
CTG	AAA	ACA	AAT	ATT	TTG	CAG	TAT	GCT	TCC	ACC	AGG	CCC	CCT	ACC	TTG	2475
Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	
	765					770					775					
TCA	CCA	ATA	CCT	CAC	ATT	CCT	CGA	AGC	CCT	TAC	AAG	TTT	CCT	AGT	TCA	2523
Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	
780					785				790						795	
CCC	TTA	CGG	ATT	CCT	GGA	GGG	AAC	ATC	TAT	ATT	TCA	CCC	CTG	AAG	AGT	2571
Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	
				800				805						810		
CCA	TAT	AAA	ATT	TCA	GAA	GGT	CTG	CCA	ACA	CCA	ACA	AAA	ATG	ACT	CCA	2619
Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	
			815					820					825			
AGA	TCA	AGA	ATC	TTA	GTA	TCA	ATT	GGT	GAA	TCA	TTC	GGG	ACT	TCT	GAG	2667
Arg	Ser	Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	
		830					835					840				
AAG	TTC	CAG	AAA	ATA	AAT	CAG	ATG	GTA	TGT	AAC	AGC	GAC	CGT	GTG	CTC	2715
Lys	Phe	Gln	Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	
	845					850					855					
AAA	AGA	AGT	GCT	GAA	GGA	AGC	AAC	CCT	CCT	AAA	CCA	CTG	AAA	AAA	CTA	2763
Lys	Arg	Ser	Ala	Glu	Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	
860					865					870					875	

CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC	2811
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu	
880 885 890	
CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT	2859
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr	
895 900 905	
CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA	2907
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser	
910 915 920	
AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT	2962
Asn Lys Glu Glu Lys	
925	
GGATTCATTG TCTCTCACAG ATGTGACTGT AT	2994

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala	1	5	10	15
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp	20	25	30	
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu	35	40	45	
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	50	55	60	
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	65	70	75	80
Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	85	90	95	
Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu	100	105	110	
Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val	115	120	125	
His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val	130	135	140	
Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	145	150	155	160



Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	165	170	175
Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	180	185	190
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	195	200	205
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	210	215	220
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	225	230	235
Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	245	250	255
Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	260	265	270
Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	275	280	285
Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	290	295	300
Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	305	310	315
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	325	330	335
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	340	345	350
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	355	360	365
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	370	375	380
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	385	390	395
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	405	410	415
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	420	425	430
Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	435	440	445
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	450	455	460
Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	465	470	475
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala			

485								490					495					
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu			
			500					505					510					
Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe			
		515					520					525						
Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg			
	530					535					540							
Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser			
545					550					555					560			
Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser			
				565					570					575				
Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu			
			580					585					590					
Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser			
		595					600					605						
Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser			
	610					615					620							
Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys			
625					630					635					640			
Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg			
				645					650					655				
Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu			
			660					665					670					
His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu			
		675					680					685						
Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met			
	690					695					700							
Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys			
705					710					715					720			
Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln			
				725					730					735				
Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile			
			740					745					750					
Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile			
		755					760					765						
Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His			
	770					775					780							
Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro			
785					790					795					800			
Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser			
			805						810					815				

Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu
			820					825					830		
Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile
		835					840					845			
Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu
	850					855					860				
Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu
865					870					875					880
Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys
				885					890					895	
Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln
			900					905					910		
Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys
		915					920					925			